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<141> 2000-10-27

<151> 1998-10-09

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<211> 29

<212> DNA

<213> Artificial sequence

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<223> MSH3 specific primer S51 for PCR using cDNA of Arabidopsis thaliana ecotype Columbia

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<211> 24

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<400> 12

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<220>
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<210> 16
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<220>
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atg ggc aag caa aag cag cag acg att tct cgt ttc ttc gct ccc aaa 147
Met Gly Lys Gln Lys Gln Gln Thr Ile Ser Arg Phe Phe Ala Pro Lys
  1             5             10             15

ccc aaa tcc ccg act cac gaa ccg aat ccg gta gcc gaa tca tca aca 195
Pro Lys Ser Pro Thr His Glu Pro Asn Pro Val Ala Glu Ser Ser Thr
             20             25             30

ccg cca ccg aag ata tcc gcc act gta tcc ttc tct cct tcc aag cgt 243
Pro Pro Pro Lys Ile Ser Ala Thr Val Ser Phe Ser Pro Ser Lys Arg
             35             40             45

aag ctt ctc tcc gac cac ctc gcc gcc gcg tca ccc aaa aag cct aaa 291
Lys Leu Leu Ser Asp His Leu Ala Ala Ala Ser Pro Lys Lys Pro Lys
             50             55             60

ctt tct cct cac act caa aac cca gta ccc gat ccc aat tta cac caa 339
Leu Ser Pro His Thr Gln Asn Pro Val Pro Asp Pro Asn Leu His Gln
             65             70             75             80

aga ttt ctc cag aga ttt ctg gaa ccc tcg ccg gag gaa tat gtt ccc 387
Arg Phe Leu Gln Arg Phe Leu Glu Pro Ser Pro Glu Glu Tyr Val Pro
             85             90             95

gaa acg tca tca tcg agg aaa tac aca cca ttg gaa cag caa gtg gtg 435
Glu Thr Ser Ser Ser Arg Lys Tyr Thr Pro Leu Glu Gln Gln Val Val
             100             105             110

gag cta aag agc aag tac cca gat gtg gtt ttg atg gtg gaa gtt ggt 483
Glu Leu Lys Ser Lys Tyr Pro Asp Val Val Leu Met Val Glu Val Gly
             115             120             125

tac agg tac aga ttc ttc gga gaa gac gcg gag atc gca gca cgc gtg 531
Tyr Arg Tyr Arg Phe Phe Gly Glu Asp Ala Glu Ile Ala Ala Arg Val
             130             135             140

ttg ggt att tac gct cat atg gat cac aat ttc atg acg gcg agt gtg 579
Leu Gly Ile Tyr Ala His Met Asp His Asn Phe Met Thr Ala Ser Val
             145             150             155             160

cca aca ttt cga ttg aat ttc cat gtg aga aga ctg gtg aat gca gga 627

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Tyr	Lys	Ile	Gly	Val	Val	Lys	Gln	Thr	Glu	Thr	Ala	Ala	Ile	Lys	Ser		
			180					185					190				
cat	ggg	gca	aac	cgg	acc	ggc	cct	ttt	ttc	cgg	gga	ctg	tcg	gcg	ttg	723	
His	Gly	Ala	Asn	Arg	Thr	Gly	Pro	Phe	Phe	Arg	Gly	Leu	Ser	Ala	Leu		
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tat	acc	aaa	gcc	acg	ctt	gaa	gcg	gct	gag	gat	ata	agt	ggg	ggg	tgt	771	
Tyr	Thr	Lys	Ala	Thr	Leu	Glu	Ala	Ala	Glu	Asp	Ile	Ser	Gly	Gly	Cys		
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Ser	Phe	Asp	Val	Arg	Val	Gly	Val	Val	Gly	Val	Glu	Ile	Ser	Thr	Gly		
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gaa	ggt	ggt	tat	gaa	gag	ttc	aat	gat	aat	ttc	atg	aga	agt	gga	tta	963	
Glu	Val	Val	Tyr	Glu	Glu	Phe	Asn	Asp	Asn	Phe	Met	Arg	Ser	Gly	Leu		
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gag	gct	gtg	att	ttg	agc	ttg	tca	cca	gct	gag	ctg	ttg	ctt	ggc	cag	1011	
Glu	Ala	Val	Ile	Leu	Ser	Leu	Ser	Pro	Ala	Glu	Leu	Leu	Leu	Gly	Gln		
	290					295					300						
cct	ctt	tca	caa	caa	act	gag	aag	ttt	ttg	gtg	gca	cat	gct	gga	cct	1059	
Pro	Leu	Ser	Gln	Gln	Thr	Glu	Lys	Phe	Leu	Val	Ala	Met	Ala	Gly	Pro		
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acc	tca	aac	ggt	cga	gtg	gaa	cgt	gcc	tca	ctg	gat	tgt	ttc	agc	aat	1107	
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Gly	Asn	Ala	Val	Asp	Glu	Val	Ile	Ser	Leu	Cys	Glu	Lys	Ile	Ser	Ala		
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aac aca gag atg act ctc tca gcc aat act ctg caa cag ttg gag gtt	1395						
Asn Thr Glu Met Thr Leu Ser Ala Asn Thr Leu Gln Gln Leu Glu Val		420		425		430	
gtg aaa aat aat tca gat gga tgc gaa tct ggc tcc tta ttc cat aat	1443						
Val Lys Asn Asn Ser Asp Gly Ser Glu Ser Gly Ser Leu Phe His Asn		435		440		445	
atg aat cac aca ctt aca gta tat gct tcc agg ctt ctt aga cac tgg	1491						
Met Asn His Thr Leu Thr Val Tyr Gly Ser Arg Leu Leu Arg His Trp		450		455		460	
gtg act cat cct cta tgc gat aga aat ttg ata tct gct cgg ctt gat	1539						
Val Thr His Pro Leu Cys Asp Arg Asn Leu Ile Ser Ala Arg Leu Asp		465		470		475	480
gct gtt tct gag att tct gct tgc atg gga tct cat agt tct tcc cag	1587						
Ala Val Ser Glu Ile Ser Ala Cys Met Gly Ser His Ser Ser Ser Gln		485		490		495	
ctc agc agt gag ttg gtt gaa gaa ggt tct gag aga gca att gta tca	1635						
Leu Ser Ser Glu Leu Val Glu Glu Gly Ser Glu Arg Ala Ile Val Ser		500		505		510	
cct gag ttt tat ctc gtg ctc tcc tca gtc ttg aca gct atg tct aga	1683						
Pro Glu Phe Tyr Leu Val Leu Ser Ser Val Leu Thr Ala Met Ser Arg		515		520		525	
tca tct gat att caa cgt gga ata aca aga atc ttt cat cgg act gct	1731						
Ser Ser Asp Ile Gln Arg Gly Ile Thr Arg Ile Phe His Arg Thr Ala		530		535		540	
aaa gcc aca gag ttc att gca gtt atg gaa gct att tta ctt gcg ggg	1779						
Lys Ala Thr Glu Phe Ile Ala Val Met Glu Ala Ile Leu Leu Ala Gly		545		550		555	560
aag caa att cag cgg ctt ggc ata aag caa gac tct gaa atg agg agt	1827						
Lys Gln Ile Gln Arg Leu Gly Ile Lys Gln Asp Ser Glu Met Arg Ser		565		570		575	
atg caa tct gca act gtg cga tct act ctt ttg aga aaa ttg att tct	1875						
Met Gln Ser Ala Thr Val Arg Ser Thr Leu Leu Arg Lys Leu Ile Ser		580		585		590	
gtt att tca tcc cct gtt gtg gtt gac aat gcc gga aaa ctt ctc tct	1923						
Val Ile Ser Ser Pro Val Val Val Asp Asn Ala Gly Lys Leu Leu Ser		595		600		605	
gcc cta aat aag gaa gcg gct gtt cga ggt gac ttg ctc gac ata cta	1971						
Ala Leu Asn Lys Glu Ala Ala Val Arg Gly Asp Leu Leu Asp Ile Leu		610		615		620	

atc act tcc agc gac caa ttt cct gag ctt gct gaa gct cgc caa gca	2019
Ile Thr Ser Ser Asp Gln Phe Pro Glu Leu Ala Glu Ala Arg Gln Ala	
625 630 635 640	
gtt tta gtc atc agg gaa aag ctg gat tcc tcg ata gct tca ttt cgc	2067
Val Leu Val Ile Arg Glu Lys Leu Asp Ser Ser Ile Ala Ser Phe Arg	
645 650 655	
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Lys Lys Leu Ala Ile Arg Asn Leu Glu Phe Leu Gln Val Ser Gly Ile	
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aca cat ttg ata gag ctg ccc gtt gat tcc aag gtc cct atg aat tgg	2163
Thr His Leu Ile Glu Leu Pro Val Asp Ser Lys Val Pro His Asn Trp	
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Val Lys Val Asn Ser Thr Lys Lys Thr Ile Arg Tyr His Pro Pro Glu	
690 695 700	
ata gta gct ggc ttg gat gag cta gct cta gca act gaa cat ctt gcc	2259
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Tyr Tyr Thr Asp Phe Lys Ala Ala Val Gln Ala Leu Ala Leu Asp	
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Cys Leu His Ser Leu Ser Thr Leu Ser Arg Asn Lys Asn Tyr Val Arg	
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ccc gag ttt gtg gat gac tgt gaa cca gtt gag ata aac ata cag tct	2451
Pro Glu Phe Val Asp Asp Cys Glu Pro Val Glu Ile Asn Ile Gln Ser	
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785 790 795 800	
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Gly Pro Asn Met Gly Gly Lys Ser Cys Tyr Ile Arg Gln Val Ala Leu	
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Ile Ser Ile Met Ala Gln Val Gly Ser Phe Val Pro Ala Ser Phe Ala	
835 840 845	

aag ctg cac gtg ctt gat ggt gtt ttc act cgg atg ggt gct tca gac	2691
Lys Leu His Val Leu Asp Gly Val Phe Thr Arg Met Gly Ala Ser Asp	
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Ser Ile Gln His Gly Arg Ser Thr Phe Leu Glu Glu Leu Ser Glu Ala	
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Glu Leu Gly Arg Gly Thr Ser Thr His Asp Gly Val Ala Ile Ala Tyr	
900 905 910	
gca aca tta cag cat ctc cta gca gaa aag aga tgt ttg gtt ctt ttt	2883
Ala Thr Leu Gln His Leu Leu Ala Glu Lys Arg Cys Leu Val Leu Phe	
915 920 925	
gtc acg cat tac cct gaa ata gct gag atc agt aac gga ttc cca ggt	2931
Val Thr His Tyr Pro Glu Ile Ala Glu Ile Ser Asn Gly Phe Pro Gly	
930 935 940	
tct gtt ggg aca tac cat gtc tcg tat ctg aca ttg cag aag gat aaa	2979
Ser Val Gly Thr Tyr His Val Ser Tyr Leu Thr Leu Gln Lys Asp Lys	
945 950 955 960	
ggc agt tat gat cat gat gat gtg acc tac cta tat aag ctt gtg cgt	3027
Gly Ser Tyr Asp His Asp Asp Val Thr Tyr Leu Tyr Lys Leu Val Arg	
965 970 975	
ggc agt tat gat cat gat gat gtg acc tac cta tat aag ctt gtg cgt	3075
Gly Leu Cys Ser Arg Ser Phe Gly Phe Lys Val Ala Gln Leu Ala Gln	
980 985 990	
ata cct cca tca tgt ata cgt cga gcc att tca atg gct gca aaa ttg	3123
Ile Pro Pro Ser Cys Ile Arg Arg Ala Ile Ser Met Ala Ala Lys Leu	
995 1000 1005	
gaa gct gag gta cgt gca aga gag aga aat aca cgc atg gga gaa cca	3171
Glu Ala Glu Val Arg Ala Arg Glu Arg Asn Thr Arg Met Gly Glu Pro	
1010 1015 1020	
gaa gga cat gaa gaa ccg aga ggc gca gaa gaa tct att tcg gct cta	3219
Glu Gly His Glu Glu Pro Arg Gly Ala Glu Glu Ser Ile Ser Ala Leu	
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ggc agt tat gat cat gat gat gtg acc tac cta tat aag ctt gtg cgt	3267
Gly Asp Leu Phe Ala Asp Leu Lys Phe Ala Leu Ser Glu Glu Asp Pro	
1045 1050 1055	
tgg aaa gca ttc gag ttt tta aag cat gct tgg aag att gct ggc aaa	3315
Trp Lys Ala Phe Glu Phe Leu Lys His Ala Trp Lys Ile Ala Gly Lys	
1060 1065 1070	
atc aga cta aaa cca act tgt tca ttt tgatttaatc ttaacattat	3362

Ile Arg Leu Lys Pro Thr Cys Ser Phe
1075 1080

agcaactgca aggtcttgat catctgtag ttgcgtacta acttatgtgt attagtataa 3422
caagaaaaga gaattagaga gatggattct aatccggtgt tgcagtacat cttttctcca 3482
ccgcataaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 3522

<210> 19
<211> 1081
<212> PRT
<213> Arabidopsis thaliana ecotype Columbia
<223> Polypeptide MSH3

<400> 19

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20 25 30
Pro Pro Pro Lys Ile Ser Ala Thr Val Ser Phe Ser Pro Ser Lys Arg
35 40 45
Lys Leu Leu Ser Asp His Leu Ala Ala Ala Ser Pro Lys Lys Pro Lys
50 55 60
Leu Ser Pro His Thr Gln Asn Pro Val Pro Asp Pro Asn Leu His Gln
65 70 75 80
Arg Phe Leu Gln Arg Phe Leu Glu Pro Ser Pro Glu Glu Tyr Val Pro
85 90 95
Glu Thr Ser Ser Arg Lys Tyr Thr Pro Leu Glu Gln Gln Val Val
100 105 110
Glu Leu Lys Ser Lys Tyr Pro Asp Val Val Leu Met Val Glu Val Gly
115 120 125
Tyr Arg Tyr Arg Phe Phe Gly Glu Asp Ala Glu Ile Ala Ala Arg Val
130 135 140
Leu Gly Ile Tyr Ala His Met Asp His Asn Phe Met Thr Ala Ser Val
145 150 155 160
Pro Thr Phe Arg Leu Asn Phe His Val Arg Arg Leu Val Asn Ala Gly
165 170 175
Tyr Lys Ile Gly Val Val Lys Gln Thr Glu Thr Ala Ala Ile Lys Ser
180 185 190
His Gly Ala Asn Arg Thr Gly Pro Phe Phe Arg Gly Leu Ser Ala Leu
195 200 205
Tyr Thr Lys Ala Thr Leu Glu Ala Ala Glu Asp Ile Ser Gly Gly Cys
210 215 220

Gly	Gly	Glu	Glu	Gly	Phe	Gly	Ser	Gln	Ser	Asn	Phe	Leu	Val	Cys	Val		
225					230					235					240		
Val	Asp	Glu	Arg	Val	Lys	Ser	Glu	Thr	Leu	Gly	Cys	Gly	Ile	Glu	Met		
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Ser	Phe	Asp	Val	Arg	Val	Gly	Val	Val	Gly	Val	Glu	Ile	Ser	Thr	Gly		
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Glu	Val	Val	Tyr	Glu	Glu	Phe	Asn	Asp	Asn	Phe	Met	Arg	Ser	Gly	Leu		
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Glu	Ala	Val	Ile	Leu	Ser	Leu	Ser	Pro	Ala	Glu	Leu	Leu	Leu	Gly	Gln		
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Pro	Leu	Ser	Gln	Gln	Thr	Glu	Lys	Phe	Leu	Val	Ala	Met	Ala	Gly	Pro		
305					310					315					320		
Thr	Ser	Asn	Val	Arg	Val	Glu	Arg	Ala	Ser	Leu	Asp	Cys	Phe	Ser	Asn		
			325					330						335			
Gly	Asn	Ala	Val	Asp	Glu	Val	Ile	Ser	Leu	Cys	Glu	Lys	Ile	Ser	Ala		
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	355						360					365					
Gly	Met	Ser	Cys	Leu	Thr	Val	His	Thr	Ile	Met	Asn	Met	Pro	His	Leu		
370						375					380						
Thr	Val	Gln	Ala	Leu	Ala	Leu	Thr	Phe	Cys	His	Leu	Lys	Gln	Phe	Gly		
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Phe	Glu	Arg	Ile	Leu	Tyr	Gln	Gly	Ala	Ser	Phe	Arg	Ser	Leu	Ser	Ser		
			405					410					415				
Asn	Thr	Glu	Met	Thr	Leu	Ser	Ala	Asn	Thr	Leu	Gln	Gln	Leu	Glu	Val		
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Val	Lys	Asn	Asn	Ser	Asp	Gly	Ser	Glu	Ser	Gly	Ser	Leu	Phe	His	Asn		
	435					440						445					
Met	Asn	His	Thr	Leu	Thr	Val	Tyr	Gly	Ser	Arg	Leu	Leu	Arg	His	Trp		
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Val	Thr	His	Pro	Leu	Cys	Asp	Arg	Asn	Leu	Ile	Ser	Ala	Arg	Leu	Asp		
465				470					475					480			
Ala	Val	Ser	Glu	Ile	Ser	Ala	Cys	Met	Gly	Ser	His	Ser	Ser	Ser	Gln		
			485					490					495				
Leu	Ser	Ser	Glu	Leu	Val	Glu	Glu	Gly	Ser	Glu	Arg	Ala	Ile	Val	Ser		
		500						505					510				
Pro	Glu	Phe	Tyr	Leu	Val	Leu	Ser	Ser	Val	Leu	Thr	Ala	Met	Ser	Arg		
	515					520						525					

Ser	Ser	Asp	Ile	Gln	Arg	Gly	Ile	Thr	Arg	Ile	Phe	His	Arg	Thr	Ala	
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Lys	Ala	Thr	Glu	Phe	Ile	Ala	Val	Met	Glu	Ala	Ile	Leu	Leu	Ala	Gly	
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Lys	Gln	Ile	Gln	Arg	Leu	Gly	Ile	Lys	Gln	Asp	Ser	Glu	Met	Arg	Ser	
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Met	Gln	Ser	Ala	Thr	Val	Arg	Ser	Thr	Leu	Leu	Arg	Lys	Leu	Ile	Ser	
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Val	Ile	Ser	Ser	Pro	Val	Val	Val	Asp	Asn	Ala	Gly	Lys	Leu	Leu	Ser	
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Ala	Leu	Asn	Lys	Glu	Ala	Ala	Val	Arg	Gly	Asp	Leu	Leu	Asp	Ile	Leu	
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Ile	Thr	Ser	Ser	Asp	Gln	Phe	Pro	Glu	Leu	Ala	Glu	Ala	Arg	Gln	Ala	
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Val	Leu	Val	Ile	Arg	Glu	Lys	Leu	Asp	Ser	Ser	Ile	Ala	Ser	Phe	Arg	
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Lys	Lys	Leu	Ala	Ile	Arg	Asn	Leu	Glu	Phe	Leu	Gln	Val	Ser	Gly	Ile	
			660					665					670			
Thr	His	Leu	Ile	Glu	Leu	Pro	Val	Asp	Ser	Lys	Val	Pro	His	Asn	Trp	
		675					680					685				
Val	Lys	Val	Asn	Ser	Thr	Lys	Lys	Thr	Ile	Arg	Tyr	His	Pro	Pro	Glu	
		690				695					700					
Ile	Val	Ala	Gly	Leu	Asp	Glu	Leu	Ala	Leu	Ala	Thr	Glu	His	Leu	Ala	
705					710					715					720	
Ile	Val	Asn	Arg	Ala	Ser	Trp	Asp	Ser	Phe	Leu	Lys	Ser	Phe	Ser	Arg	
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Tyr	Tyr	Thr	Asp	Phe	Lys	Ala	Ala	Val	Gln	Ala	Leu	Ala	Ala	Leu	Asp	
			740					745					750			
Cys	Leu	His	Ser	Leu	Ser	Thr	Leu	Ser	Arg	Asn	Lys	Asn	Tyr	Val	Arg	
		755					760					765				
Pro	Glu	Phe	Val	Asp	Asp	Cys	Glu	Pro	Val	Glu	Ile	Asn	Ile	Gln	Ser	
		770				775					780					
Gly	Arg	His	Pro	Val	Leu	Glu	Thr	Ile	Leu	Gln	Asp	Asn	Phe	Val	Pro	
785					790					795					800	
Asn	Asp	Thr	Ile	Leu	His	Ala	Glu	Gly	Glu	Tyr	Cys	Gln	Ile	Ile	Thr	
				805					810					815		
Gly	Pro	Asn	Met	Gly	Gly	Lys	Ser	Cys	Tyr	Ile	Arg	Gln	Val	Ala	Leu	
			820					825					830			

Ile Ser Ile Met Ala Gln Val Gly Ser Phe Val Pro Ala Ser Phe Ala
 835 840 845
 Lys Leu His Val Leu Asp Gly Val Phe Thr Arg Met Gly Ala Ser Asp
 850 855 860
 Ser Ile Gln His Gly Arg Ser Thr Phe Leu Glu Glu Leu Ser Glu Ala
 865 870 875 880
 Ser His Ile Ile Arg Thr Cys Ser Ser Arg Ser Leu Val Ile Leu Asp
 885 890 895
 Glu Leu Gly Arg Gly Thr Ser Thr His Asp Gly Val Ala Ile Ala Tyr
 900 905 910
 Ala Thr Leu Gln His Leu Leu Ala Glu Lys Arg Cys Leu Val Leu Phe
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 Val Thr His Tyr Pro Glu Ile Ala Glu Ile Ser Asn Gly Phe Pro Gly
 930 935 940
 Ser Val Gly Thr Tyr His Val Ser Tyr Leu Thr Leu Gln Lys Asp Lys
 945 950 955 960
 Gly Ser Tyr Asp His Asp Asp Val Thr Tyr Leu Tyr Lys Leu Val Arg
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 Gly Leu Cys Ser Arg Ser Phe Gly Phe Lys Val Ala Gln Leu Ala Gln
 980 985 990
 Ile Pro Pro Ser Cys Ile Arg Arg Ala Ile Ser Met Ala Ala Lys Leu
 995 1000 1005
 Glu Ala Glu Val Arg Ala Arg Glu Arg Asn Thr Arg Met Gly Glu Pro
 1010 1015 1020
 Glu Gly His Glu Glu Pro Arg Gly Ala Glu Glu Ser Ile Ser Ala Leu
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 Gly Asp Leu Phe Ala Asp Leu Lys Phe Ala Leu Ser Glu Glu Asp Pro
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<210> 20

<211> 24

<212> DNA

<213> Artificial sequence

<220>

<223> MSH6 specific primer 638 for PCR using cDNA of Arabidopsis thaliana

ecotype Columbia

<400> 20

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<210> 21

<211> 28

<212> DNA

<213> Artificial sequence

<220>

<223> Primer S81 for PCR using cDNA of Arabidopsis thaliana ecotype Columbia

<400> 21

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<210> 22

<211> 30

<212> DNA

<213> Artificial sequence

<220>

<223> MSH6 specific primer S823 for PCR using cDNA of Arabidopsis thaliana ecotype Columbia

<400> 22

gcttggcgca tctaatagaa tcatgacagg 30

<210> 23

<211> 24

<212> DNA

<213> Artificial sequence

<220>

<223> MSH6 specific primer 637 for PCR using cDNA of Arabidopsis thaliana ecotype Columbia

<400> 23

gacagcgtca gttcttcaga atgc 24

<210> 24

<211> 33

<212> DNA

<213> Artificial sequence

<220>

<223> MSH6 specific primer 1S8 for PCR using cDNA of Arabidopsis thaliana ecotype Columbia

<400> 24

atccccgggat gcagcgccag agatcgattt tgt 33

<210> 25

<211> 27

<212> DNA

<213> Artificial sequence

<220>

<223> MSH6 specific primer S83 for PCR using cDNA of Arabidopsis thaliana ecotype Columbia

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<210> 26

<211> 2188

<212> DNA

<213> Arabidopsis thaliana ecotype Columbia

<223> Clone 43

<400> 26

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gttgtttccgc	tgaatgattc	atctctatgt	atgaaggcta	atgatgttat	tcctcaattt	420
cgttccaata	atggtaaaac	tcaagaaaga	aaccatgctt	ttagtttcag	tgggagagct	480
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cttctgggga	aaaaagtgt	gaaacaacga	gttaaagcat	ttgggcaa	tgtgaaagg	2040
ttcagaagt	gaattgatct	gttgttggt	ctacagaagg	aatcaaatat	gatgagttg	2100
ctttataaac	tctgtaaact	tcctatatta	gtaggaaaaa	gcgggctaga	gttatttctt	2160
tctcaattcg	aagcagccat	agatagcg				2188

<210> 27
 <211> 1385
 <212> DNA
 <213> Arabidopsis thaliana ecotype Columbia
 <223> Clone 62

<400> 27

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tcaccaagga	attcgcgtct	caccacgtg	tcacctcgaa	acacatggct	tgccgattca	1020
aatcaagatc	tgattatcaa	ccacgtggtt	gtgatcaaga	cctagtgttc	ttgtaccgtt	1080
taaccgaggg	agcttgtcct	gagagctacg	gacttcaagt	ggcactcatg	gctggaatac	1140
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ccggg					1385	

<210> 28
 <211> 34
 <212> DNA
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<220>
 <223> MSH6 specific primer 2S8 for PCR using cDNA of Arabidopsis thaliana ecotype Columbia

<400> 28

atccccgggtt atttgggaac acagtaagag gatt 34

<210> 29
 <211> 27
 <212> DNA
 <213> Artificial sequence

<220>
 <223> MSH6 specific primer S82 for PCR using cDNA of Arabidopsis thaliana ecotype Columbia

<400> 29

gcgttcgatc atcagcctct gtgttgc 27

<210> 30
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 <212> DNA
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<220>
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tctctctcac aattccaaaa a atg cag cgc cag aga tcg att ttg tct ttc 171
 Met Gln Arg Gln Arg Ser Ile Leu Ser Phe
 1 5 10

ttc caa aaa ccc acc gcg gcg act acg aag ggt ttg gtt tcc ggc gat 219
 Phe Gln Lys Pro Thr Ala Ala Thr Thr Lys Gly Leu Val Ser Gly Asp
 15 20 25

gct gct agc ggc ggg ggc ggc agc gga gga cca cga ttt aat gtg aag 267
 Ala Ala Ser Gly Gly Gly Ser Gly Gly Pro Arg Phe Asn Val Arg
 30 35 40

gaa ggg gat gct aaa ggc gac gct tct gta cgt ttt gct gtt tcg aaa 315
 Glu Gly Asp Ala Lys Gly Asp Ala Ser Val Arg Phe Ala Val Ser Lys
 45 50 55

tct gtc gat gag gtt aga gga acg gat act cca ccg gag aag gtt ccg 363
 Ser Val Asp Glu Val Arg Gly Thr Asp Thr Pro Pro Glu Lys Val Pro
 60 65 70

cgt cgt gtc ctg ccg tct gga ttt aag ccg gct gaa tcc gcc gst gat 411
 Arg Arg Val Leu Pro Ser Gly Phe Lys Pro Ala Glu Ser Ala Gly Asp
 75 80 85 90

gct tcg tcc ctg ttc tcc aat att atg cat aag ttt gta aaa gtc gat 459
 Ala Ser Ser Leu Phe Ser Asn Ile Met His Lys Phe Val Lys Val Asp
 95 100 105

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Asp	Arg	Asp	Cys	Ser	Gly	Glu	Arg	Ser	Arg	Glu	Asp	Val	Val	Pro	Leu	
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aat	gat	tca	tct	cta	tgt	atg	aag	gct	aat	gat	gtt	att	cct	caa	ttt	555
Asn	Asp	Ser	Ser	Leu	Cys	Met	Lys	Ala	Asn	Asp	Val	Ile	Pro	Gln	Phe	
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Arg	Ser	Asn	Asn	Gly	Lys	Thr	Gln	Glu	Arg	Asn	His	Ala	Phe	Ser	Phe	
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agt	ggg	aga	gct	gaa	ctt	aga	tca	gta	gaa	gat	ata	gga	gta	gat	ggc	651
Ser	Gly	Arg	Ala	Glu	Leu	Arg	Ser	Val	Glu	Asp	Ile	Gly	Val	Asp	Gly	
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Asp	Val	Pro	Gly	Pro	Glu	Thr	Pro	Gly	Met	Arg	Pro	Arg	Ala	Ser	Arg	
			175					180						185		
ttg	aag	cga	gtt	ctg	gag	gat	gaa	atg	act	ttt	aag	gag	gat	aag	gtt	747
Leu	Lys	Arg	Val	Leu	Glu	Asp	Glu	Met	Thr	Phe	Lys	Glu	Asp	Lys	Val	
		190					195					200				
cct	gta	ttg	gac	tct	aac	aaa	agg	ctg	aaa	atg	ctc	cag	gat	ccg	gtt	795
Pro	Val	Leu	Asp	Ser	Asn	Lys	Arg	Leu	Lys	Met	Leu	Gln	Asp	Pro	Val	
		205					210				215					
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Cys	Gly	Glu	Lys	Lys	Glu	Val	Asn	Glu	Gly	Thr	Lys	Phe	Glu	Trp	Leu	
	220					225					230					
gag	tct	tct	cga	atc	agg	gat	gcc	aat	aga	aga	cgt	cct	gat	gat	ccc	891
Glu	Ser	Ser	Arg	Ile	Arg	Asp	Ala	Asn	Arg	Arg	Arg	Pro	Asp	Asp	Pro	
235					240				245						250	
ctt	tac	gat	aga	aag	acc	tta	cac	ata	cca	cct	gat	gtt	ttc	aag	aaa	939
Leu	Tyr	Asp	Arg	Lys	Thr	Leu	His	Ile	Pro	Pro	Asp	Val	Phe	Lys	Lys	
				255				260						265		
atg	tct	gca	tca	caa	aag	caa	tat	tgg	agt	gtt	aag	agt	gaa	tat	atg	987
Met	Ser	Ala	Ser	Gln	Lys	Gln	Tyr	Trp	Ser	Val	Lys	Ser	Glu	Tyr	Met	
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gac	att	gtg	ctt	ttc	ttt	aaa	gtg	ggg	aaa	ttt	tat	gag	ctg	tat	gag	1035
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cta	gat	gcg	gaa	tta	ggg	cac	aag	gag	ctt	gac	tgg	aag	atg	acc	atg	1083
Leu	Asp	Ala	Glu	Leu	Gly	His	Lys	Glu	Leu	Asp	Trp	Lys	Met	Thr	Met	
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agt	ggg	gtg	gga	aaa	tgc	aga	cag	gtt	ggg	atc	tct	gaa	agt	ggg	ata	1131
Ser	Gly	Val	Gly	Lys	Cys	Arg	Gln	Val	Gly	Ile	Ser	Glu	Ser	Gly	Ile	
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gat gag gca gtg caa aag cta tta gct cgt gga tat aaa gtt gga cga	1179
Asp Glu Ala Val Gln Lys Leu Leu Ala Arg Gly Tyr Lys Val Gly Arg	
335 340 345	
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Ile Glu Gln Leu Glu Thr Ser Asp Gln Ala Lys Ala Arg Gly Ala Asn	
350 355 360	
act ata att cca agg aag cta gtt cag gta tta act cca tca aca gca	1275
Thr Ile Ile Pro Arg Lys Leu Val Gln Val Leu Thr Pro Ser Thr Ala	
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Ser Glu Gly Asn Ile Gly Pro Asp Ala Val His Leu Leu Ala Ile Lys	
380 385 390	
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Glu Ile Lys Met Glu Leu Gln Lys Cys Ser Thr Val Tyr Gly Phe Ala	
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Phe Val Asp Cys Ala Ala Leu Arg Phe Trp Val Gly Ser Ile Ser Asp	
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Asp Ala Ser Cys Ala Ala Leu Gly Ala Leu Leu Met Gln Val Ser Pro	
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Lys Glu Val Leu Tyr Asp Ser Lys Gly Leu Ser Arg Glu Ala Gln Lys	
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gct cta agg aaa tat acg ttg aca ggg tct acg gcg gta cag ttg gct	1563
Ala Leu Arg Lys Tyr Thr Leu Thr Gly Ser Thr Ala Val Gln Leu Ala	
460 465 470	
cca gta cca caa gta atg ggg gat aca gat gct gct gga gtt aga aat	1611
Pro Val Pro Gln Val Met Gly Asp Thr Asp Ala Ala Gly Val Arg Asn	
475 480 485 490	
ata ata gaa tct aac gga tac ttt aaa ggt tct tct gaa tca tgg aac	1659
Ile Ile Glu Ser Asn Gly Tyr Phe Lys Gly Ser Ser Glu Ser Trp Asn	
495 500 505	
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Cys Ala Val Asp Gly Leu Asn Glu Cys Asp Val Ala Leu Ser Ala Leu	
510 515 520	
gga gag cta att aat cat ctg tct agg cta aag cta gaa gat gta ctt	1755
Gly Glu Leu Ile Asn His Leu Ser Arg Leu Lys Leu Glu Asp Val Leu	
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Lys His Gly Asp Ile Phe Pro Tyr Gln Val Tyr Arg Gly Cys Leu Arg	
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att gat ggc cag acg atg gta aat ctt gag ata ttt aac aat agc tgt	1851

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Asp	Gly	Gly	Pro	Ser	Gly	Thr	Leu	Tyr	Lys	Tyr	Leu	Asp	Asn	Cys	Val	
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agt	cca	act	ggg	aag	cga	ctc	tta	agg	aat	tgg	atc	tgc	cat	cca	ctc	1947
Ser	Pro	Thr	Gly	Lys	Arg	Leu	Leu	Arg	Asn	Trp	Ile	Cys	His	Pro	Leu	
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aaa	gat	gta	gaa	agc	atc	aat	aaa	cgg	ctt	gat	gta	gtt	gaa	gaa	ttc	1995
Lys	Asp	Val	Glu	Ser	Ile	Asn	Lys	Arg	Leu	Asp	Val	Val	Glu	Glu	Phe	
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Thr	Ala	Asn	Ser	Glu	Ser	Met	Gln	Ile	Thr	Gly	Gln	Tyr	Leu	His	Lys	
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Ser	Ser	Ala	Ser	Val	Leu	Pro	Ala	Leu	Leu	Gly	Lys	Lys	Val	Leu	Lys	
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caa	cga	gtt	aaa	gca	ttt	ggg	caa	att	gtg	aaa	ggg	ttc	aga	agt	gga	2187
Gln	Arg	Val	Lys	Ala	Phe	Gly	Gln	Ile	Val	Lys	Gly	Phe	Arg	Ser	Gly	
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Ile	Asp	Leu	Leu	Ala	Leu	Gln	Lys	Glu	Ser	Asn	Met	Met	Ser	Leu		
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ctt	tat	aaa	ctc	tgt	aaa	ctt	cct	ata	tta	gta	gga	aaa	agc	ggg	cta	2283
Leu	Tyr	Lys	Leu	Cys	Lys	Leu	Pro	Ile	Leu	Val	Gly	Lys	Ser	Gly	Leu	
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gag	tta	ttt	ctt	tct	caa	ttc	gaa	gca	gcc	ata	gat	agc	gac	ttt	cca	2331
Glu	Leu	Phe	Leu	Ser	Gln	Phe	Glu	Ala	Ala	Ile	Asp	Ser	Asp	Phe	Pro	
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Asn	Tyr	Gln	Asn	Gln	Asp	Val	Thr	Asp	Glu	Asn	Ala	Glu	Thr	Leu	Thr	
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Ile	His	Thr	Ile	Ser	Cys	Leu	Asp	Val	Leu	Arg	Ser	Phe	Ala	Ile	Ala	
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Ser Glu Ala Thr Asp Gln Asn Gln Lys Thr Lys Gly Pro Ile Leu Lys			
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atc caa gga cta tgg cat cca ttt gca gtt gca gcc gat ggt caa ttg	2619		
Ile Gln Gly Leu Trp His Pro Phe Ala Val Ala Ala Asp Gly Gln Leu			
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Pro Val Pro Asn Asp Ile Leu Leu Gly Glu Ala Arg Arg Ser Ser Gly			
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Lys Ser Thr Leu Leu Arg Ala Thr Cys Leu Ala Val Ile Phe Ala Gln			
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ctt ggc tgc tac gtg ccg tgt gag tct tgc gaa atc tcc ctc gtg gat	2811		
Leu Gly Cys Tyr Val Pro Cys Glu Ser Cys Glu Ile Ser Leu Val Asp			
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gta gag aaa gtt caa tgt ccg atg ctc ttt gca aca cat tac cac cct	3051		
Val Glu Lys Val Gln Cys Arg Met Leu Phe Ala Thr His Tyr His Pro			
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ctc acc aag gaa ttc gcg tct cac cca cgt gtc acc tcg aaa cac atg	3099		
Leu Thr Lys Glu Phe Ala Ser His Pro Arg Val Thr Ser Lys His Met			
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gct tgc gca ttc aaa tca aga tct gat tat caa cca cgt ggt tgt gat	3147		
Ala Cys Ala Phe Lys Ser Arg Ser Asp Tyr Gln Pro Arg Gly Cys Asp			
	990	995	1000
caa gac cta gtg ttc ttg tac cgt tta acc gag gga gct tgt cct gag	3195		
Gln Asp Leu Val Phe Leu Tyr Arg Leu Thr Glu Gly Ala Cys Pro Glu			
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1035 1040 1045 1050

gga aac ttc aag tca agt gag cta aga tct gag ttc tca agt ctg cat 3339
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gaa gac tgg ctc aag tca ttg gtg ggt att tct cga gtc gcc cac aac 3387
Glu Asp Trp Leu Lys Ser Leu Val Gly Ile Ser Arg Val Ala His Asn
1070 1075 1080

aat gcc ccc att ggc gaa gat gac tac gac act ttg ttt tgc tta tgg 3435
Asn Ala Pro Ile Gly Glu Asp Asp Tyr Asp Thr Leu Phe Cys Leu Trp
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His Glu Ile Lys Ser Ser Tyr Cys Val Pro Lys
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tgacataaca ctatctgaag ctcgttaagt cttttgcctc tctgatgttt attcctotta 3538
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<400> 31

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Gly Ser Gly Gly Pro Arg Phe Asn Val Arg Glu Gly Asp Ala Lys Gly
35 40 45

Asp Ala Ser Val Arg Phe Ala Val Ser Lys Ser Val Asp Glu Val Arg
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Gly Thr Asp Thr Pro Pro Glu Lys Val Pro Arg Arg Val Leu Pro Ser
65 70 75 80

Gly Phe Lys Pro Ala Glu Ser Ala Gly Asp Ala Ser Ser Leu Phe Ser
85 90 95

Asn Ile Met His Lys Phe Val Lys Val Asp Asp Arg Asp Cys Ser Gly

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Asp	Glu	Met	Thr	Phe	Lys	Glu	Asp	Lys	Val	Pro	Val	Leu	Asp	Ser	Asn						
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Asp	Ala	Asn	Arg	Arg	Arg	Pro	Asp	Asp	Pro	Leu	Tyr	Asp	Arg	Lys	Thr						
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Gln	Tyr	Trp	Ser	Val	Lys	Ser	Glu	Tyr	Met	Asp	Ile	Val	Leu	Phe	Phe						
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Lys	Val	Gly	Lys	Phe	Tyr	Glu	Leu	Tyr	Glu	Leu	Asp	Ala	Glu	Leu	Gly						
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 <223> Forward primer DMCIN-A for PCR on genomic DNA of Arabidopsis thaliana ssp. Landsberg erecta "Ler"

<400> 34

gaagcgatat tgttcgtg 18

<210> 35
<211> 18
<212> DNA
<213> Artificial sequence

<220>
<223> Reverse primer DMCIN-B for PCR on genomic DNA of *Arabidopsis thaliana* ssp. *Landsberg erecta* "Ler"

<400> 35

agattgcgag aacattcc 18

<210> 36
<211> 31
<212> DNA
<213> Artificial sequence

<220>
<223> Forward primer DMCIN-1 for PCR on genomic DNA of *Arabidopsis thaliana* ssp. *Landsberg erecta* "Ler"

<400> 36

acgcgctcgac tcagctatga gattactcgt g 31

<210> 37
<211> 29
<212> DNA
<213> Artificial sequence

<220>
<223> Reverse primer DMCIN-2 for PCR on genomic DNA of *Arabidopsis thaliana* ssp. *Landsberg erecta* "Ler"

<400> 37

gctctagatt tctcgctcta agactctct 29

<210> 38
<211> 32
<212> DNA
<213> Artificial sequence

<220>
<223> Forward primer DMCIN-3 for PCR on genomic DNA of *Arabidopsis thaliana* ssp. *Landsberg erecta* "Ler"

<400> 38

gctctagagc ttctcttaag taagtgattg at 32

<210> 39

<211> 48

<212> DNA

<213> Artificial sequence

<220>

<223> Reverse primer DMCIN-4 for PCR on genomic DNA of *Arabidopsis thaliana* ssp. *Landsberg erecta* "Ler"

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tcccccgggc tcgagagatc tccatgggtt cttcagctct atgaatcc 48

<210> 40

<211> 26

<212> DNA

<213> Artificial sequence

<220>

<223> Forward primer DMC1a for PCR on genomic DNA of *Arabidopsis thaliana* ssp. *Landsberg erecta* "Ler"

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acgcgtcgac gaattcgcaa gtgggg 26

<210> 41

<211> 38

<212> DNA

<213> Artificial sequence

<220>

<223> Reverse primer DMC1b for PCR on genomic DNA of *Arabidopsis thaliana* ssp. *Landsberg erecta* "Ler"

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<210> 42

<211> 20

<212> DNA

<213> Artificial sequence

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<223> Forward primer for PCR amplification of ATEAT1 SSLP marker in *Arabidopsis thaliana* subspecies

<400> 42

gccactgcgt gaatgatatg 20

<210> 43
<211> 22
<212> DNA
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<220>
<223> Reverse primer for PCR amplification of ATEAT1 SSLP marker in
Arabidopsis thaliana subspecies

<400> 43

cgaacagcca acattaattc cc 22

<210> 44
<211> 18
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<223> Forward primer for PCR amplification of NGA63 SSLP marker in
Arabidopsis
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<400> 44

aaccaaggca cagaagcg 18

<210> 45
<211> 18
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thaliana subspecies

<400> 45

acccaagtga tcgccacc 18

<210> 46
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Arabidopsis thaliana subspecies

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taccgaacca aaacacaaaag g 21

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<211> 22

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<223> Reverse primer for PCR amplification of NGA248 SSLP marker in
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tctgtatctc ggtgaattct cc 22

<210> 48

<211> 22

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<223> Forward primer for PCR amplification of NGA128 SSLP marker in
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<210> 49

<211> 22

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<210> 50

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Arabidopsis thaliana subspecies

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Arabidopsis thaliana subspecies

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ccttcacatc caaaacccac 20

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Arabidopsis thaliana subspecies

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gcacataccc acaaccagaa 20

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aaagagatga gaatttggac 20

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Arabidopsis thaliana subspecies

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<223> Forward primer for PCR amplification of AthUBIQUE SSLP marker in
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aggcaaattgt ccatttcatt g 21

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<223> Reverse primer for PCR amplification of AthUBIQUE SSLP marker in
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<400> 65

acgacatggc agatttctcc 20

<210> 66
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Arabidopsis thaliana subspecies

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agctgcttcc ttatagcgtc c 21

<210> 67
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 catccgaatg ccattgttc 19

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 gaaaaaacgc tactttcgtg g 21

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 caagagcaat atcaagagca gc 22

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 catgcaattt gcatctgagg 20

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<211> 22
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ctctgtcact cttttcctct gg 22

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thaliana subspecies

<400> 72

tggatttctt cctctcttca c 21

<210> 73
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thaliana subspecies

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thaliana subspecies

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thaliana subspecies

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Arabidopsis
thaliana subspecies

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gagggcaaat ctttatttcg g 21

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Arabidopsis
thaliana subspecies

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Arabidopsis thaliana subspecies

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gcgaaaaaac aaaaaaatcc a 21

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cgacgaatcg acagaattag g 21

<210> 80
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Arabidopsis thaliana subspecies

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gaaatccaaa tcccagagag g 21

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Arabidopsis thaliana subspecies

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tctccccact agttttgtgt cc 22

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taccgtcaat ttcacgcc 19

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Arabidopsis thaliana subspecies

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<400> 84

aatcccagta accaaacaca ca 22

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Arabidopsis
thaliana subspecies

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cccagtctaa ccacgaccac 20

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Arabidopsis thaliana subspecies

<400> 86

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<210> 87
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Arabidopsis thaliana subspecies

<400> 88

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<210> 89
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Arabidopsis thaliana subspecies

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thaliana subspecies

<400> 93

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<223> Forward primer for PCR amplification of ATHSO191 SSLP marker in
Arabidopsis thaliana subspecies

<400> 94

ctccaccaat catgcaaag 20

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<223> Forward primer for PCR amplification of NGA129 SSLP marker in
Arabidopsis thaliana subspecies

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<210> 97
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 35 40 45
 Thr His Lys Gln Glu Gln Glu Val Ala Val Gly Asn Gly Ala Gly Ser
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 Glu Ser Ile Cys Leu Asp Thr Asp Glu Glu Asp Asn Leu Ser Ser Val
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 Ala Ser Thr Thr Val Thr Asn Asp Ser Phe Pro Leu Lys Gly Ser Val
 85 90 95
 Ser Ser Lys Asn Ser Lys Asn Ser Glu Lys Thr Ser Gly Thr Ser Thr
 100 105 110
 Thr Phe Asn Asp Ile Asp Phe Ala Lys Lys Leu Asp Arg Ile Met Lys
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 Arg Arg Ser Asp Glu Asn Val Glu Ala Glu Asp Asp Glu Glu Glu Gly
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 Glu Glu Asp Phe Val Lys Lys Lys Ala Arg Lys Ser Pro Thr Ala Lys
 145 150 155 160
 Leu Thr Pro Leu Asp Lys Gln Val Lys Asp Leu Lys Met His His Arg
 165 170 175
 Asp Lys Val Leu Val Ile Arg Val Gly Tyr Lys Tyr Lys Cys Phe Ala
 180 185 190
 Glu Asp Ala Val Thr Val Ser Arg Ile Leu His Ile Lys Leu Val Pro
 195 200 205
 Gly Lys Leu Thr Ile Asp Glu Ser Asn Pro Gln Asp Cys Asn His Arg
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 Gln Phe Ala Tyr Cys Ser Phe Pro Asp Val Arg Leu Asn Val His Leu
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 Glu Arg Leu Val His His Asn Leu Lys Val Ala Val Val Glu Gln Ala
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 Glu Thr Ser Ala Ile Lys Lys His Asp Pro Gly Ala Ser Lys Ser Ser
 260 265 270
 Val Phe Glu Arg Lys Ile Ser Asn Val Phe Thr Lys Ala Thr Phe Gly
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 Val Asn Ser Thr Phe Val Leu Arg Gly Lys Arg Ile Leu Gly Asp Thr
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 305 310 315 320
 Lys Tyr Ser Leu Ile Ser Val Asn Leu Asn Asn Gly Glu Val Val Tyr
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Asp Glu Phe Glu Glu Pro Asn Leu Ala Asp Glu Lys Leu Gln Ile Arg
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 Ile Lys Tyr Leu Gln Pro Ile Glu Val Leu Val Asn Thr Asp Asp Leu
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 Pro Leu His Val Ala Lys Phe Phe Lys Asp Ile Ser Cys Pro Leu Ile
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 His Lys Gln Glu Tyr Asp Leu Glu Asp His Val Val Gln Ala Ile Lys
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 Val Met Asn Glu Lys Ile Gln Leu Ser Pro Ser Leu Ile Arg Leu Val
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 Ser Lys Leu Tyr Ser His Met Val Glu Tyr Asn Asn Glu Gln Val Met
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 Leu Ile Pro Ser Ile Tyr Ser Pro Phe Ala Ser Lys Ile His Met Leu
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 Gly Lys Gly Ser Leu Phe Trp Leu Leu Asp His Thr Arg Thr Ser Phe
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 Gly Leu Arg Met Leu Arg Glu Trp Ile Leu Lys Pro Leu Val Asp Val
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 His Gln Ile Glu Glu Arg Leu Asp Ala Ile Glu Cys Ile Thr Ser Glu
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 Asp His Phe Lys Met His Gln Ser Tyr Leu Ser Glu His Phe Lys Ser
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 Thr Met Ile Asn Val Ser Ala Val Met Glu Lys Asn Ser Asp Lys Gln
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 Val Met Asp Phe Phe Asn Leu Asn Asn Tyr Asp Cys Ser Glu Gly Ile
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 Tyr Lys Asp Leu Leu Ile Arg Glu Ser Glu Leu Gln Tyr Lys Glu Phe
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Gly	Lys	Val	Val	Asp	Ser	Glu	Ser	Asp	Glu	Asp	Glu	Tyr	Leu	Pro	Asp
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Lys	Asn	Asp	Gly	Asp	Glu	Asp	Asp	Asp	Ile	Ala	Asp	Asp	Lys	Glu	Asp
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Leu	Val	Glu	Ala	Val	Lys	Ser	Trp	Thr	Asn	Ala	Phe	Glu	Arg	Gln	Lys	
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785					790					795					800	
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Thr	Tyr	Lys	Arg	Tyr	Tyr	Ser	Asp	Glu	Val	Arg	Ala	Leu	Ala	Arg	Ser	
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Asn	Arg	Leu	Cys	Gln	Lys	Phe	Asp	Ala	His	Tyr	Asn	Thr	Ile	Trp	Met	
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Pro	Thr	Ile	Gln	Ala	Ile	Ser	Asn	Ile	Asp	Cys	Leu	Leu	Ala	Ile	Thr	
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	915						920					925				
Asp	Glu	Val	Asp	Ser	Lys	Thr	Asn	Thr	Gln	Leu	Asn	Gly	Phe	Leu	Lys	
	930					935					940					
Phe	Lys	Ser	Leu	Arg	His	Pro	Cys	Phe	Asn	Leu	Gly	Ala	Thr	Thr	Ala	
945					950					955					960	
Lys	Asp	Phe	Ile	Pro	Asn	Asp	Ile	Glu	Leu	Gly	Lys	Glu	Gln	Pro	Arg	
			965					970						975		
Leu	Gly	Leu	Leu	Thr	Gly	Ala	Asn	Ala	Ala	Gly	Lys	Ser	Thr	Ile	Leu	
		980					985						990			
Arg	Met	Ala	Cys	Ile	Ala	Val	Ile	Met	Ala	Gln	Met	Gly	Cys	Tyr	Val	
	995						1000					1005				
Pro	Cys	Glu	Ser	Ala	Val	Leu	Thr	Pro	Ile	Asp	Arg	Ile	Met	Thr	Arg	
	1010					1015					1020					
Leu	Gly	Ala	Asn	Asp	Asn	Ile	Met	Gln	Gly	Lys	Ser	Thr	Phe	Phe	Val	
1025					1030					1035					1040	

Glu	Leu	Ala	Glu	Thr	Lys	Lys	Ile	Leu	Asp	Met	Ala	Thr	Asn	Arg	Ser
				1045					1050					1055	
Leu	Leu	Val	Val	Asp	Glu	Leu	Gly	Arg	Gly	Gly	Ser	Ser	Ser	Asp	Gly
			1060					1065						1070	
Phe	Ala	Ile	Ala	Glu	Ser	Val	Leu	His	His	Val	Ala	Thr	His	Ile	Gln
			1075					1080					1085		
Ser	Leu	Gly	Phe	Phe	Ala	Thr	His	Tyr	Gly	Thr	Leu	Ala	Ser	Ser	Phe
			1090					1095				1100			
Lys	His	His	Pro	Gln	Val	Arg	Pro	Leu	Lys	Met	Ser	Ile	Leu	Val	Asp
1105					1110					1115					1120
Glu	Ala	Thr	Arg	Asn	Val	Thr	Phe	Leu	Tyr	Lys	Met	Leu	Glu	Gly	Gln
				1125					1130					1135	
Ser	Glu	Gly	Ser	Phe	Gly	Met	His	Val	Ala	Ser	Met	Cys	Gly	Ile	Ser
			1140						1145				1150		
Lys	Glu	Ile	Ile	Asp	Asn	Ala	Gln	Ile	Ala	Ala	Asp	Asn	Leu	Glu	His
			1155					1160				1165			
Thr	Ser	Arg	Leu	Val	Lys	Glu	Arg	Asp	Leu	Ala	Ala	Asn	Asn	Leu	Asn
						1175					1180				
Gly	Glu	Val	Val	Ser	Val	Pro	Gly	Gly	Leu	Gln	Ser	Asp	Phe	Val	Arg
1185					1190					1195					1200
Ile	Ala	Tyr	Gly	Asp	Gly	Leu	Lys	Asn	Thr	Lys	Leu	Gly	Ser	Gly	Glu
				1205					1210					1215	
Gly	Val	Leu	Asn	Tyr	Asp	Trp	Asn	Ile	Lys	Arg	Asn	Val	Leu	Lys	Ser
			1220						1225				1230		
Leu	Phe	Ser	Ile	Ile	Asp	Asp	Leu	Gln	Ser						
			1235					1240							